CTCGAGGACAGTGACCTGGGAGTGAGTACAAGGTGAGGCCACCACTCAGGGT
GCCAGCTCCAAGCGGGTCACAGGGACGAGGGCTGCGGCCATCAGGAGGCCCT
GCACACACATCTGGGACACGCGCCCCGAGGGCCAGTTCACCTCAGTGCGCC
TCATTCTCCTGCACAAAAGCGCCCCCATCCTTTCTTCACAAGGCTTTCGTGG
AAGCAGAGGCGTCGATGCCCAGTACCCTCTCCCTTTCCCAGGCAACGGGACC
CCAAGTTTGCTGACTGGGACCACCAAGCCACGCATGCGTCAAGAGTGAGAGT
CCGGGACCTAGGCAGGGGCCCTGGGGTTGGGCCTGAGAGAGAAGAGAACCTC
CCCCAGCACTCGGTGTGCATCGGTAGTGAAGGAGCCTCACCTGACCCCCGCT
GTTGCTCAATCGACTTCCCAAGAACAGAGAGAAAAGGGAACTTCCAGGGCGG
CCCGGGCCTCCTGGGGGTTCCCACCCCATTTTTAGCTGAAAGCACTGAGGCA
GAGCTCCCCCTACCCAGGCTCCACTGCCCGGCACAGAAATAACAACCACGGT
TACTGATCATCTGGGAGCTGTCCAGGAATTC

FIG._1A

```
  1  GCTGGGCTAA ACTGGGCTAG CCTGAGCTGG GCTGAACTGG GCTGCTGGGC
 51  TGGACTGGGT AAGCTGGGCT GAGCTGGGTT GGGTGGAAAT GGGCTGAGCT
101  GAGCTAGGCT AAACTGGGTT TGGCTGGGCT GGGCTGGGCT GGG
```

FIG._2B

```
  1  GGTTTGGCTG GGCTGGGCTG GGCTGGGCTG GGTTCAGCTG AGCGGGTTGG
 51  GTTAGACTGG GTCAAACTGG TTCAGC
```

FIG._2C

GERMLINE & LOCUS

IL-4 INDUCIBLE PROMOTER FRAGMENT
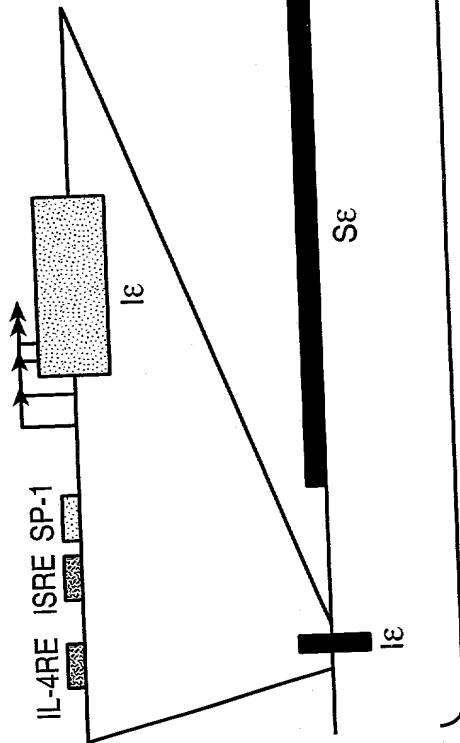
IL-4RE ISRE SP-1

ε

IL-4RE ISRE SP-1

ε

Sε

Cε

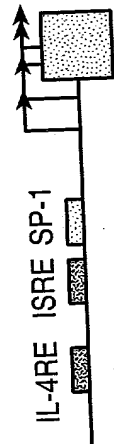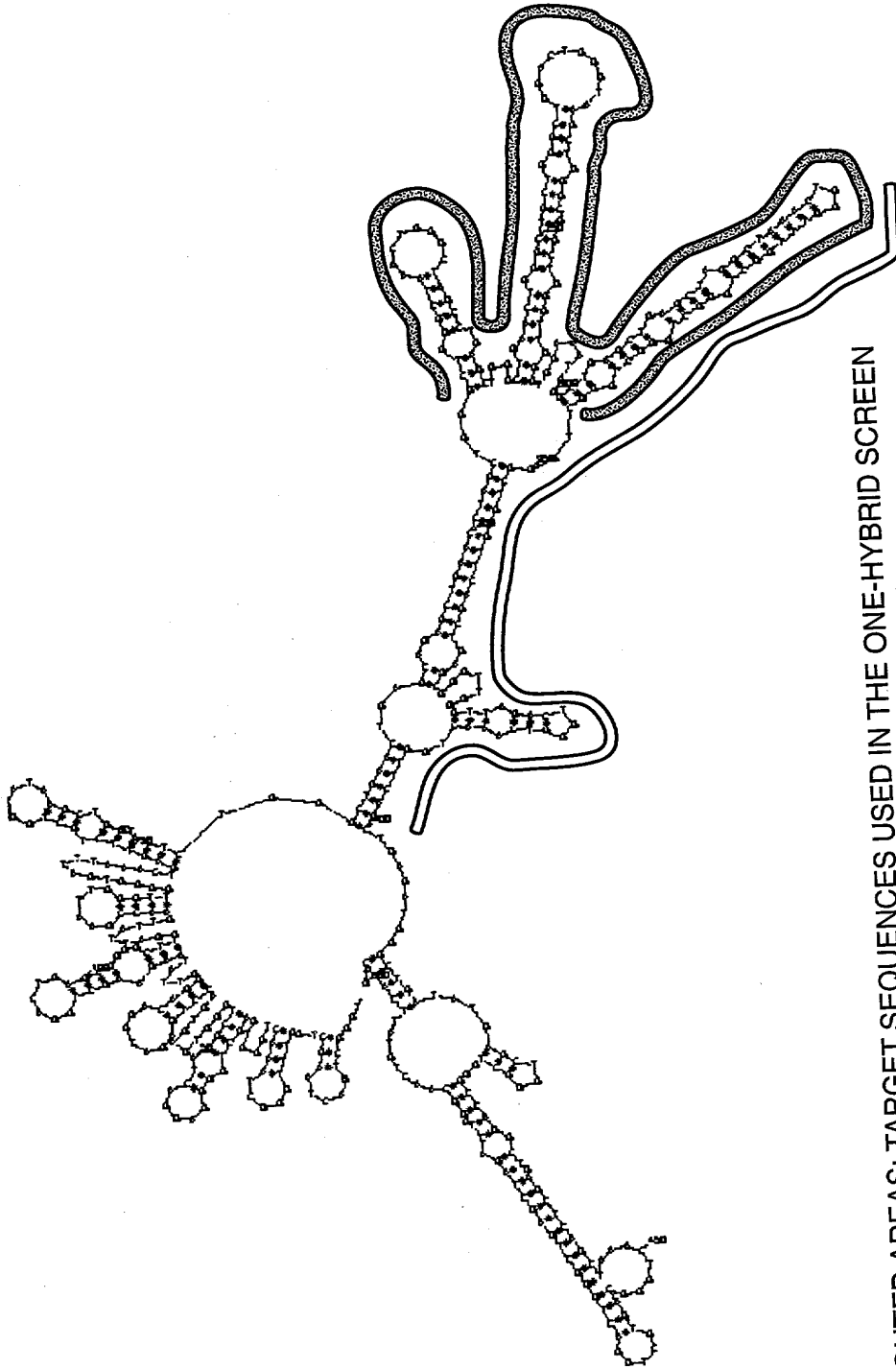FIG._1B

LOW ENERGY DNA FOLDING OF THE Sε REGION

HIGHLIGHTED AREAS: TARGET SEQUENCES USED IN THE ONE-HYBRID SCREEN

APPENDIX E

FIG._2A

YEAST ONE-HYBRID SCREENING

ONE HYBRID REPORTER VECTORS
DNA SEQUENCES OF INTEREST ARE INSERTED INTO THE MULTIPLE CLONING SITES (MCS).
THE ENZYME USED TO LINEARIZE THE VECTOR IS SHOWN WITH A SOLID ARROW.
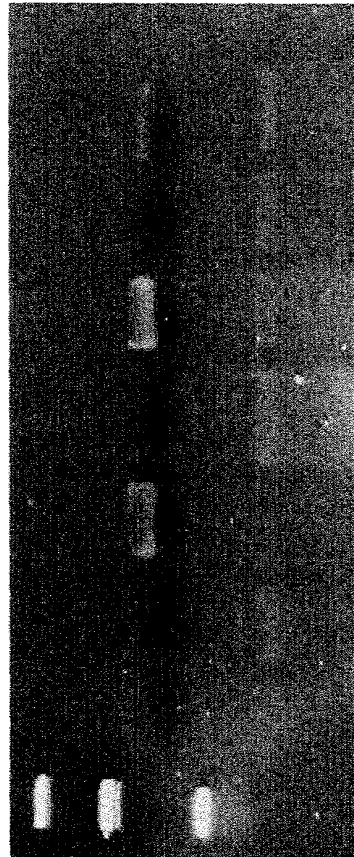DASHED ARROWS INDICATE THE TRANSCRIPTION OF THE REPORTER GENE.
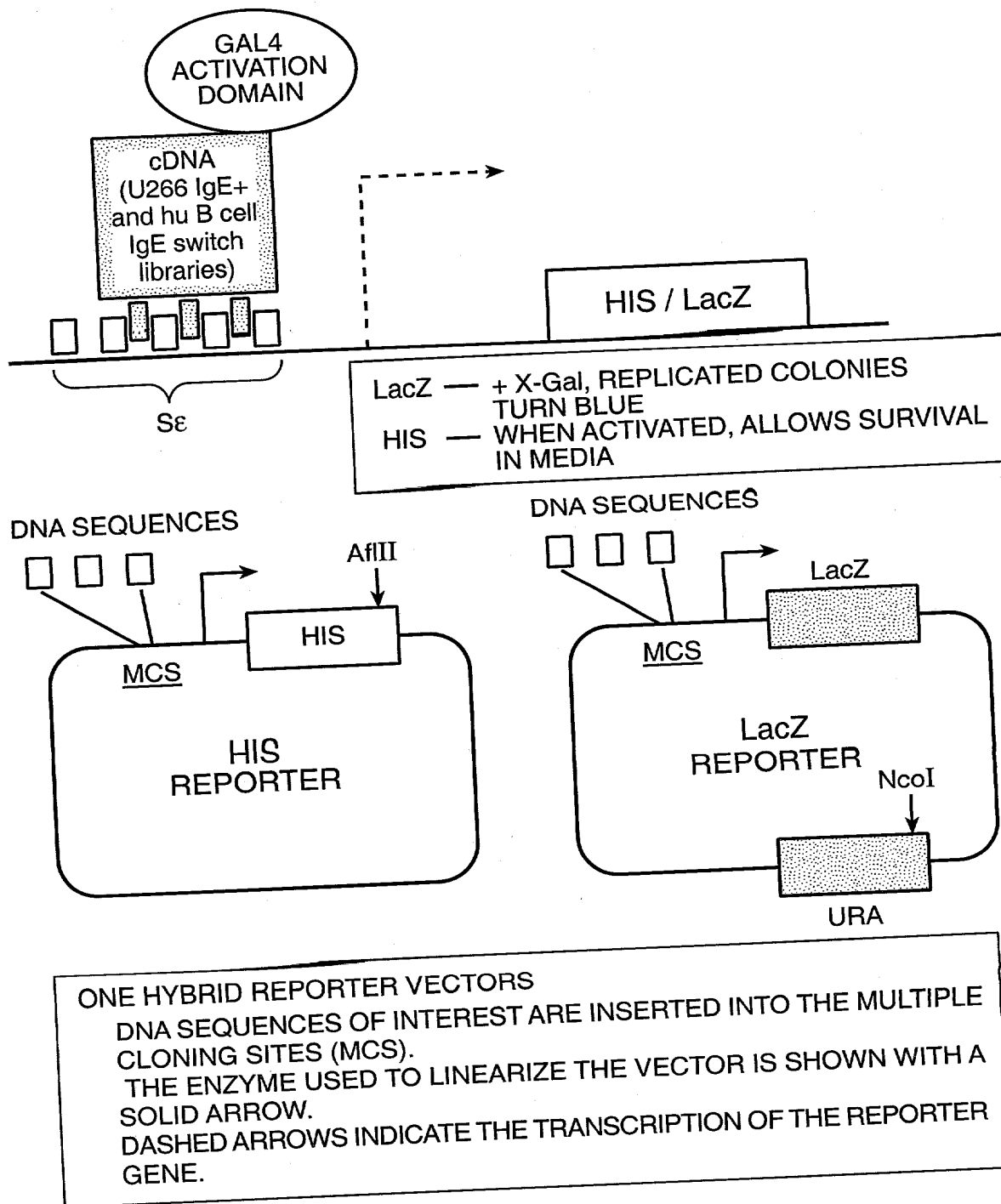
APPENDIX F

FIG._3

IL-4 INDUCTION OF GERMLINE ε mRNA IN THE
IgM + B CELL LINES: CA-46, MC-116 AND DND39

DND39 + IL-4

DND39 - IL-4

MC-116 + IL-4

MC-116 - IL-4

CA-46 + IL-4

CA-46 - IL-4

NEG. CONT.

246bp   123 bp

CELLS WERE INCUBATED FOR 48 HRS. IN 300 U / ml OF h-IL-4.
RT-PCR WAS PERFORMED USING PRIMERS SPECIFIC FOR THE GERMLINE
ε EXON AND THE 5'-END OF THE Cε CH1 EXON (PREDICTED SIZE ~ 200 bp).

APPENDIX G

FIG._4

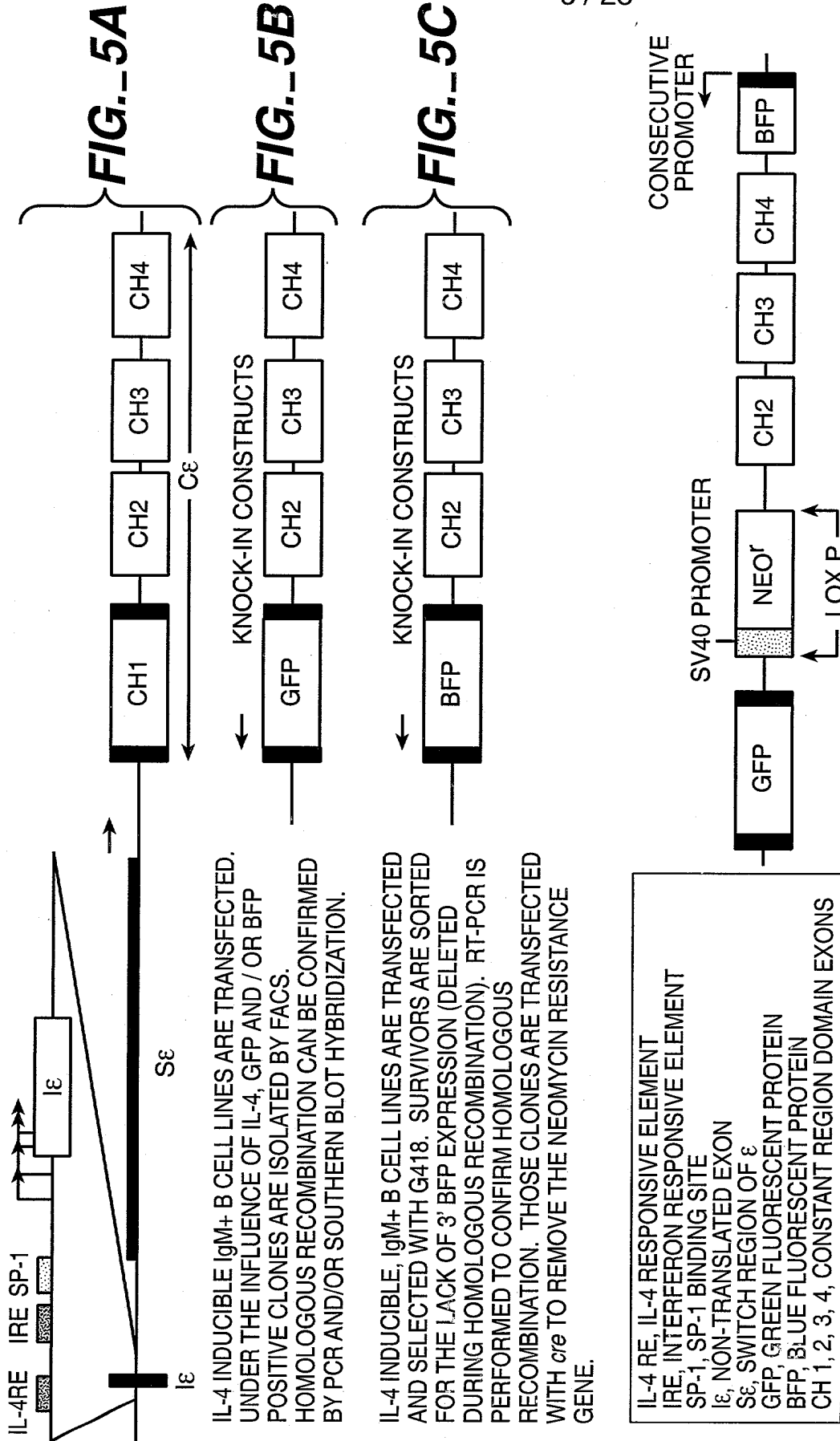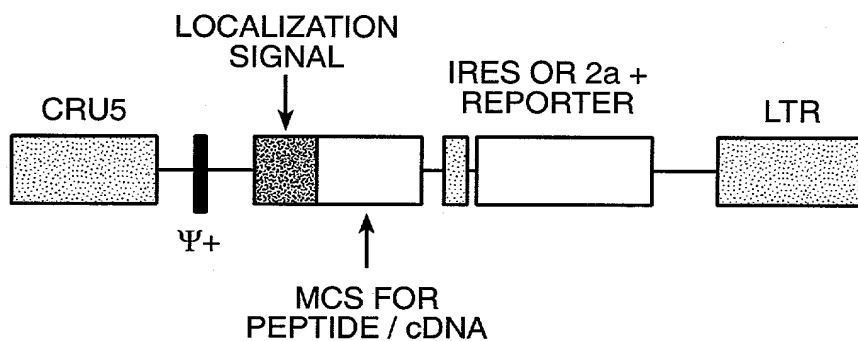APPROACHES TO GENERATE GERMLINE ε PROMOTER KNOCK-IN REPORTER CELL LINES

FIG._5A

FIG._5B

FIG._5C

FIG._5D

IL-4 INDUCIBLE IgM+ B CELL LINES ARE TRANSFECTED. UNDER THE INFLUENCE OF IL-4, GFP AND / OR BFP POSITIVE CLONES ARE ISOLATED BY FACS. HOMOLOGOUS RECOMBINATION CAN BE CONFIRMED BY PCR AND/OR SOUTHERN BLOT HYBRIDIZATION.

IL-4 INDUCIBLE, IgM+ B CELL LINES ARE TRANSFECTED AND SELECTED WITH G418. SURVIVORS ARE SORTED FOR THE LACK OF 3' BFP EXPRESSION (DELETED DURING HOMOLOGOUS RECOMBINATION). RT-PCR IS PERFORMED TO CONFIRM HOMOLOGOUS RECOMBINATION. THOSE CLONES ARE TRANSFECTED WITH cre TO REMOVE THE NEOMYCIN RESISTANCE GENE.

IL-4 RE, IL-4 RESPONSIVE ELEMENT
IRE, INTERFERON RESPONSIVE ELEMENT
SP-1, SP-1 BINDING SITE
Iε, NON-TRANSLATED EXON
Sε, SWITCH REGION OF ε
GFP, GREEN FLUORESCENT PROTEIN
BFP, BLUE FLUORESCENT PROTEIN
CH 1, 2, 3, 4, CONSTANT REGION DOMAIN EXONS
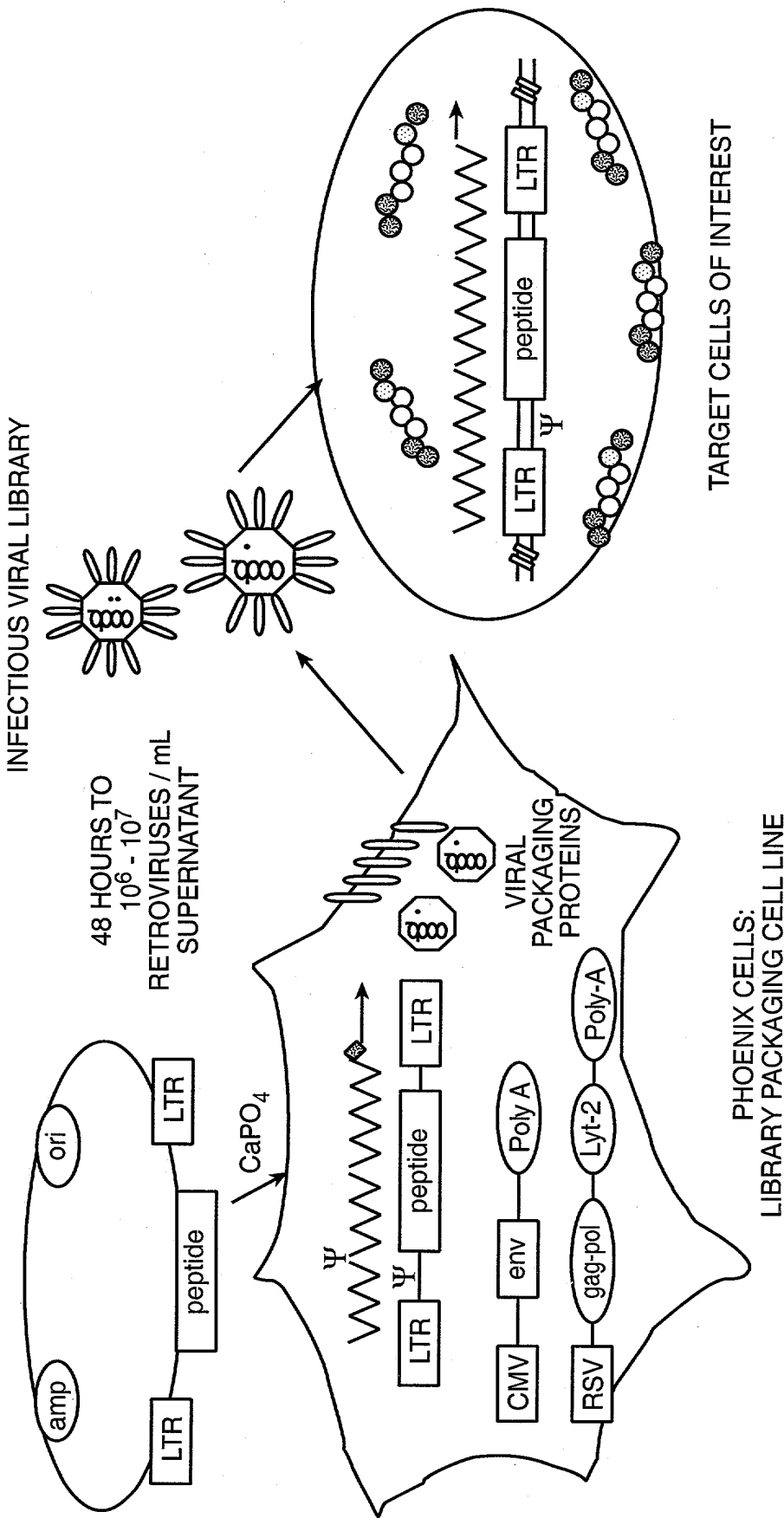
APPENDIX A

RIGEL BASE VECTOR

ALL COMPONENTS ARE UNIQUELY CASSETTED FOR FLEXIBILITY

CRU5, MODIFIED LTR
LTR, LONG TERMINAL REPEAT
$\Psi+$, PACKING SIGNAL
LOCALIZATION SIGNAL: NUCLEAR, CELL MEMBRANE, GRANULAR
MCS, MULTIPLE CLONING SITE
IRES, INTERNAL RIBOSOME ENTRY SITE
2a, SELF-CLEAVING PEPTIDE

APPENDIX I

FIG._6

PROTOCOL FOR TRANSFECTION OF PHOENIX CELLS
AND INFECTION OF NONADHERENT TARGET CELLS

INFECTIOUS VIRAL LIBRARY

48 HOURS TO
$10^6 - 10^7$
RETROVIRUSES / mL
SUPERNATANT

VIRAL PACKAGING PROTEINS

PHOENIX CELLS:
LIBRARY PACKAGING CELL LINE

TARGET CELLS OF INTEREST

FIG._7

APPENDIX I

ε HEAVY CHAIN GFP / BFP KNOCK-IN CELL LINE

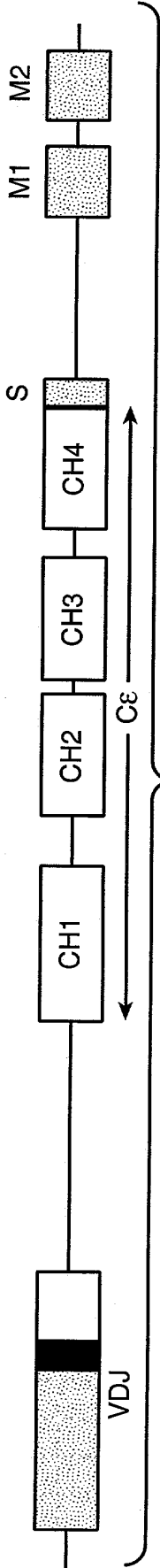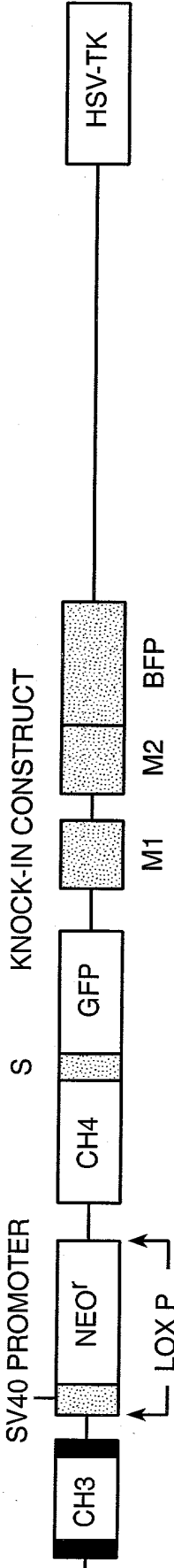U266 ε HEAVY CHAIN

FIG._8A

KNOCK-IN CONSTRUCT

FIG._8B

S, SECRETORY EXON
GFP, GREEN FLUORESCENT PROTEIN
BFP, BLUE FLUORESCENT PROTEIN
Neo^r, NEOMYCIN RESISTANCE GENE
VDJ, V REGION EXON
CH 1, 2, 3, 4, CONSTANT REGION DOMAIN EXONS
M1, M2, MEMBRANE EXONS
HSV-TK, HERPES SIMPLEX VIRUS-THYMIDINE KINASE

U266 CELLS ARE TRANSFECTED AND SELECTED WITH G418. SURVIVORS
ARE TREATED WITH GANCICLOVIR (HSV-TK DELETED DURING
HOMOLOGOUS RECOMBINATION). RT-PCR IS PERFORMED TO CONFIRM
HOMOLOGOUS RECOMBINATION. THOSE CLONES ARE TRANSFECTED
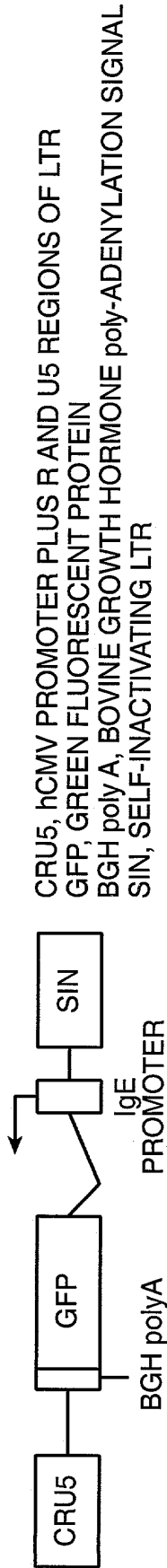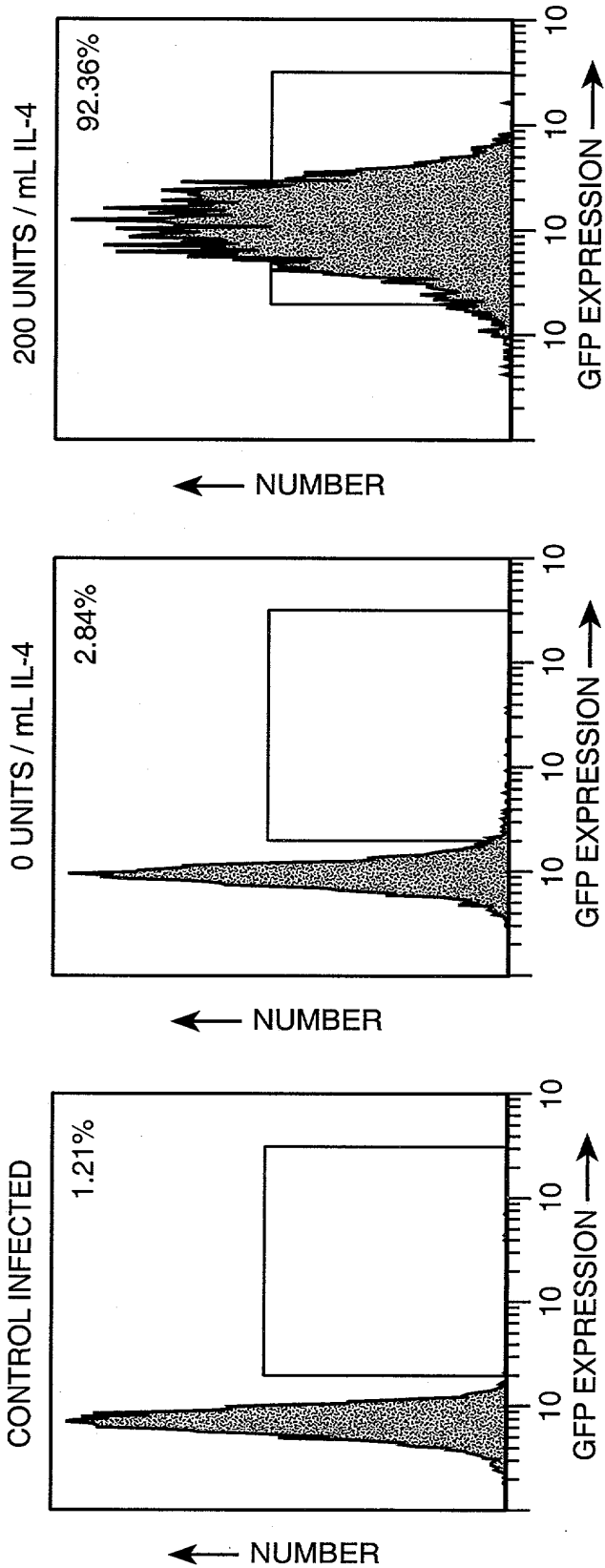WITH *cre* TO REMOVE THE SV40 NEOMYCIN RESISTANCE GENE.

APPENDIX D

IL-4 INDUCIBLE ε PROMOTER REPORTER CELL LINE

REPORTER CONSTRUCT

CRU5, hCMV PROMOTER PLUS R AND U5 REGIONS OF LTR
GFP, GREEN FLUORESCENT PROTEIN
BGH poly A, BOVINE GROWTH HORMONE poly-ADENYLATION SIGNAL
SIN, SELF-INACTIVATING LTR

IL-4 INDUCED REPORTER

200 UNITS / mL IL-4 — 92.36%

0 UNITS / mL IL-4 — 2.84%

CONTROL INFECTED — 1.21%

GFP EXPRESSION →

NUMBER ←

APPENDIX C

FIG._9A

REPORTER LINE INFECTED WITH BFP CONSTRUCT

LIBRARY CONSTRUCT

BFP, BLUE FLUORESCENT PROTEIN

CRU5 BFP LTR
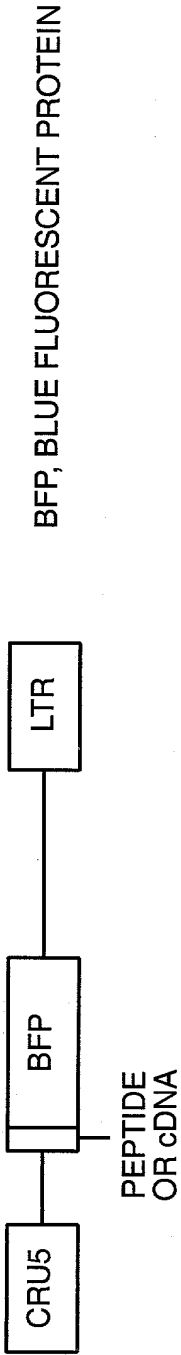
PEPTIDE
OR cDNA

FACS PROFILE OF CELLS WITH BOTH REPORTER AND PEPTIDE LIBRARY

100 U / ml IL-4

NO IL-4

BFP EXPRESSION

GFP EXPRESSION

APPENDIX C
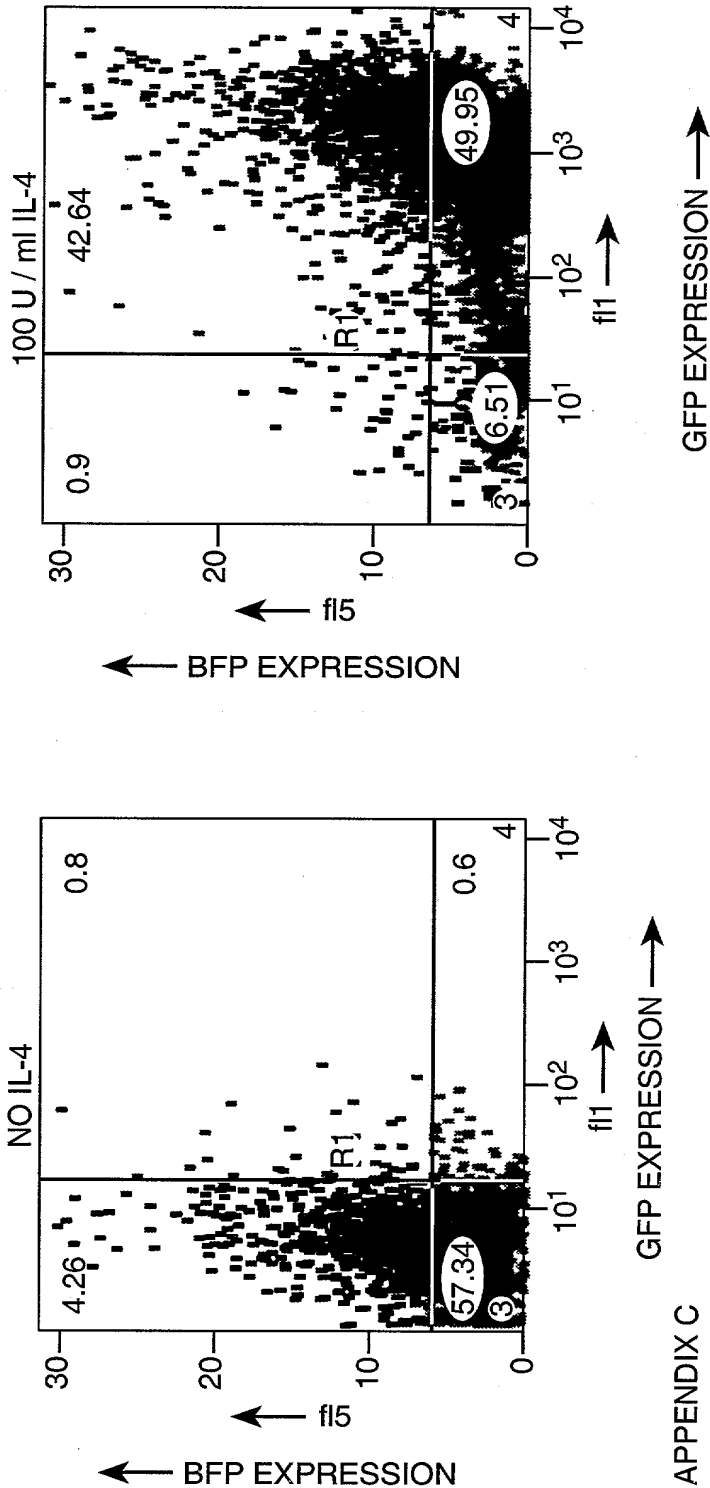
FIG._9B

SCREEN FOR PEPTIDE INHIBITORS OF THE GERMLINE ε PROMOTER

INFECTED CELLS

+ SELECTION AGENT →

REMOVAL OF LEAKY CELLS

+ IL-4 + PUROMYCIN →

SURVIVAL OF IL-4 INDUCIBLE CLONES

+ LIBRARY + IL-4 + SELECTION AGENT →

SURVIVAL OF PEPTIDE INHIBITED CLONES

SURVIVAL CONSTRUCT

SIN | LTR

Ψ+

ε GERMLINE PROMOTER

IL-4 INDUCIBLE POSITION 1

2a

PUROMYCIN OR GFP

SIN | LTR

+ DEATH INDUCER
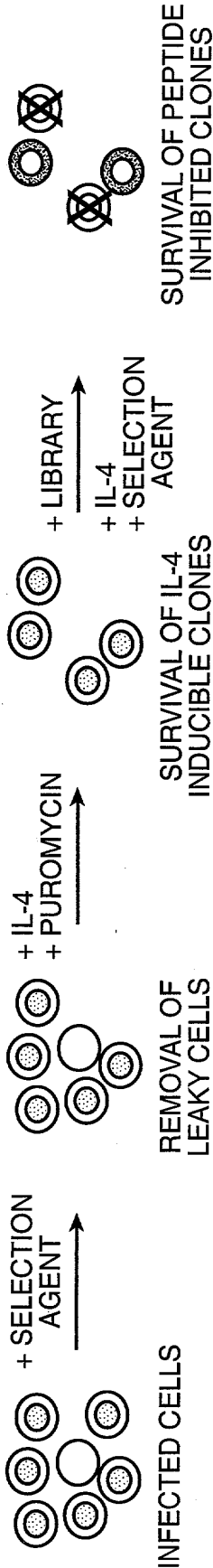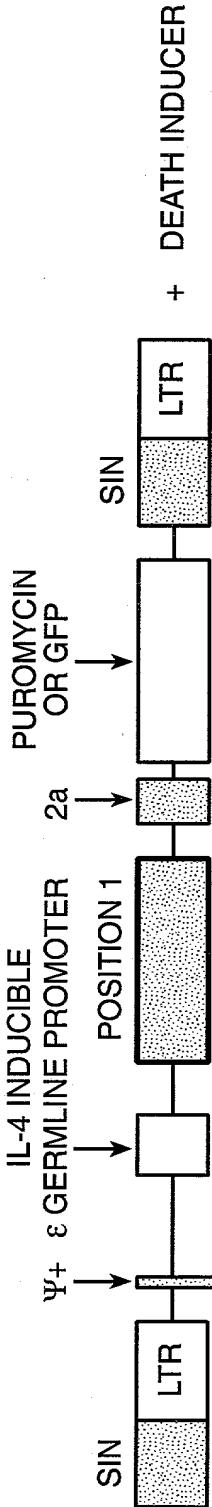
POSITION 1

FAS CHIMERIC RECEPTOR*
*(MOUSE FASK EXTERNAL / MOUSE CD8 EXTERNAL + HUMAN TRANSMEMBRANE AND CYTOPLASMIC DOMAINS)

HSV-TK

P450 2B1

p21 PEPTIDE

SELECTION AGENT

αFAS

GANCICLOVIR

CYCLOPHOSPHAMIDE

NONE (SELF SELECTION)

ALL COMPONENTS ARE CASSETED FOR FLEXIBILITY

SIN, SELF-INACTIVATING LTR
LTR, LONG TERMINAL REPEAT

APPENDIX D

FIG._10

1-845 CMV promoter/R/U5 5' LTR
1322   GAG ATG-ATC mutation
850-2100 extended Ψ region
2146-2173 two Bstx1 peptide cloning sites
2205-2723 ECMV IRES (cloned as EcoR1/Msc1 fragment from
    pCITE-4a [Novagen])
2746-3465 GFP coding region
3522-4115 3' LTR
4122-6210 pGEM backbone (pUC origin, ampR)

ATCACGAGGCCCTTTCGTCTTCAAGAACAGCTTTGCTCTTAGGAGTTTCCTAATACATCC
CAAACTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGTTATTAATAGTAATCAA
TTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAA
ATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATG
TTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
AAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTC
CTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGC
AGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCA
TTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAA
GCAGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACT
GAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGT
CTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTT
CATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCACCG
GGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGACTGA
TTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGG
TGGAACTGACGAGTTCGGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTCGG
GGGCCGTTTTTGTGGCCCGACCTGAGTCCAAAAATCCCGATCGTTTTGGACTCTTTGGTG
CACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCC
CGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGACCGAAGCCGCGCCGCGCGTCTTGTCT
GCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATA
TCGGCCCGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATG
TCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCT
GCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAG
ACCTCATCACCCAGGTTAAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACC
AGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGC
CCTTTGTACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTG
AACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAG
GCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCCGCCCCTTGTAAACTTCC
CTGACCCTGACATGACAAGAGTTACTAACAGCCCCTCTCTCCAAGCTCACTTACAGGCTC
TCTACTTAGTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACTGG
ACCGACCGGTGGTACCTCACCCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACC
AGACTAAGAACCTAGAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCCA
CCGCCCTCAAAGTAGACGGCATCGCGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGA
CCCCGGGGGGTGGACCATCCTCTAGACTGCCGGATCTCGAGGGATCCACCACCATGGACCC
CCATTAAATTGGAATTCCTGCAGCCCGGGGGGATCCACTAGTTCTAGAGCGAATTAATTCC

FIG._11A-1

GGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTG
TCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGT
TGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAG
CGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGC
CACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGA
TAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATG
CCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACAT
GTGTTAGTCGAGGTTAAAAAACGTCTAGGCCCCCGAACCACGGGGACGTGGTTTTCCT
TTGAAAAACACGATGATAATATGGGGGATCCACCGGTCGCCACCATGGTGAGCAAGGGCG
AGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCC
ACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGA
AGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGA
CCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCA
AGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCA
ACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGC
TGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACT
ACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACT
TCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGA
ACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGT
CCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGA
CCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCTCGACGA
TAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTA
GGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGA
GAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACA
GGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTG
AATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAA
CAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTC
CAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCG
CTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCC
TCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAA
ACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGA
GTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTCCGACTTGTGGTCTCGCTGCCTTGG
GAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTCACATGCAGCATGTAT
CAAAATTAATTTGGTTTTTTTTTCTTAAGTATTTACATTAAATGGCCATAGTTGCATTAAT
GAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGCGCTCTTCCGCTTCCTCGCT
CACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGC
GGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGG
CCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCG
CCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG
ACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGAC
CCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
TAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGT
GCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC
CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACAC

FIG.__11A-2

TAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT
TGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAA
GCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG
GTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAA
AAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTGCGCAAATCAATCTAAAG
TATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTC
AGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC
ACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGG
TCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAG
TAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTC
ACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTAC
ATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAG
AAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTAC
TGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTG
AGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGC
GCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACT
CTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTG
ATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAA
TGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTT
TCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATG
TATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTC

FIG._11A-3

1-845 CMVpromoter/R/U5 5' LTR
1322   GAG ATG-ATC mutation
850-2100 extended ψ region
2151-2865 GFP coding region
2866-2894 GGGSGGG linker
2895-2952 FMDV 2a cleavage sequence
2953-3004 Bstx1/Bstx1/HinD3/Hpal/Sal1/Not1 polylinker
3052-3645 3' LTR
3652-5715 pGEM backbone (pUC origin, ampR)

ATCACGAGGCCCTTTCGTCTTCAAGAACAGCTTTGCTCTTAGGAGTTTCCTAATACATC
CCAAACTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGTTATTAATAGTAATC
AATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGG
TAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACG
TATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTT
ACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTA
TTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGG
GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCG
GTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTC
TCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCA
AAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGA
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CTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCA
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TAGTGTCTATGACTGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGT
ATCTGGCGGACCCGTGGTGGAACTGACGAGTTCGGAACACCCGGCCGCAACCCTGGGAG
ACGTCCCAGGGACTTCGGGGGCCGTTTTTGTGGCCCGACCTGAGTCCAAAAATCCCGAT
CGTTTTGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGA
CGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGACCGAA
GCCGCGCCGCGCGTCTTGTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTG
TTTCTGTATTTGTCTGAAAATATCGGCCCGGGCCAGACTGTTACCACTCCCTTAAGTTT
GACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCA
AGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGG
CCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTC
ACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCTGGGAAGCCTTGG
CTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCTCTT
CCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTC
CCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCTTAT
ATGGGGCACCCCCGCCCCTTGTAAACTTCCCTGACCCTGACATGACAAGAGTTACTAAC
AGCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCACGAAGTCTGGAG
ACCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGACCGGTGGTACCTCACCCTTACC
GAGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTAGAACCTCGCTGG
AAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATCGC
AGCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTA
GACTGCCGGATCTCGAGGGATCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGG

FIG._11B-1

GTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC
CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCA
CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAG
TGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCC
CGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCC
GCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATC
GACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCA
CAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCC
GCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCC
ATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCGCCCT
GAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCG
CCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGAATTCGGAGGTGGCAGCGGTGGC
GGTCAGCTGTTGAATTTTGACCTTCTTAAACTTGCGGGAGACGTCGAGTCCAACCCTGG
GCCCACCACCACCATGGAAGCTTCCATTAAATTGGTTAACGTCGACGCGGCCGCTCGAC
GATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCT
GTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAA
CTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCC
AAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAA
CAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG
CCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCA
GATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCA
ATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGC
CCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGT
GTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAG
GGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTCCGACTTGTGGT
CTCGCTGCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTCA
CATGCAGCATGTATCAAAATTAATTTGGTTTTTTTTCTTAAGTATTTACATTAAATGGC
CATAGTTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGCGCT
CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA
TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA
GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGG
CGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAG
AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCT
CGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTT
CGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
GTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTT
ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAG
CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG
AAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT
GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCG
CTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCT
CAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACG
TTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATT
AAAAATGAAGTTTGCGCAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGT
TACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCAT
AGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCC
CCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATA

FIG._11B-2

AACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCAT
CCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCT
TCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAA
AAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGT
TATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGA
TGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCG
ACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTT
TAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCG
CTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTT
TACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGG
GAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGA
AGCATTTATCAGGGTTATTGTCTCATGACATTAACCTATAAAAATAGGCGT

FIG._11B-3

1-845 CMVpormoter/R/U5 5' LTR
1322 GAG ATG-ATC mutation
850-2100 extended ψ region
2146-2173 two Bstx1 peptide cloning sites
2173-2214 EoR1/Apa1/Hpa1/Not1 polylinker
2262-2855 3' LTR
2855-4901 pGEM backbone (pUC origin, ampR)

ATCACGAGGCCCTTTCGTCTTCAAGAACAGCTTTGCTCTTAGGAGTTTCCTAATACATC
CCAAACTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGTTATTAATAGTAATC
AATTACGGGGGTCATTAGTTCATAGCCATATATGGAGTTCCGCGTTACATAACTTACGGT
AAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGT
ATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTA
CGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTAT
TGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCT
CCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAA
AATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAG
GTCTATATAAGCAGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCC
TCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCAT
CCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTC
AGCGGGGGTCTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCA
CCGACCCACCACCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCT
AGTGTCTATGACTGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGTA
TCTGGCGGACCCGTGGTGGAACTGACGAGTTCGGAACACCCGGCCGCAACCCTGGGAGA
CGTCCCAGGGACTTCGGGGGCCGTTTTTGTGGCCCGACCTGAGTCCAAAAATCCCGATC
GTTTTGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGAC
GAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGGACCGAAG
CCGCGCCGCGCGTCTTGTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGT
TTCTGTATTTGTCTGAAAATATCGGCCCGGGCCAGACTGTTACCACTCCCTTAAGTTTG
ACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAA
GAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGC
CGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTCA
CCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCTGGGAAGCCTTGGC
TTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCTCTTC
CTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCC
CTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCTTATA
TGGGGCACCCCCGCCCCTTGTAAACTTCCCTGACCCTGACATGACAAGAGTTACTAACA
GCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCACGAAGTCTGGAGA
CCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGACCGGTGGTACCTCACCCTTACCG
AGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCTAGAACCTCGCTGGA
AAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATCGCA
GCTTGGATACACGCCGCCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTAG
ACTGCCGGATCTCGAGGGATCCACCACCATGGACCCCCATTAAATTGGAATTCGGGGCC
CAAGCTTTGTTAACGTCGACGCGGCCGCCGTCGACGATAAAATAAAAGATTTTATTTAG
TCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAG
TAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCA

FIG._11C-1

AGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAG
TTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGA
TATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATG
CGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGA
CCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTT
CGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCC
AGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGT
TGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTAC
CCGTCAGCGGGGGTCTTTCATTTCCGACTTGTGGTCTCGCTGCCTTGGGAGGGTCTCCT
CTGAGTGATTGACTACCCGTCAGCGGGGGTCTTCACATGCAGCATGTATCAAAATTAAT
TTGGTTTTTTTTCTTAAGTATTTACATTAAATGGCCATAGTTGCATTAATGAATCGGCC
AACGCGCGGGGAGAGGCGGTTTGCGTATTGGCGCTCTTCCGCTTCCTCGCTCACTGACT
CGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATA
CGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCA
AAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC
CTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTA
TAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT
GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATA
GCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTG
CACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC
CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA
GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG
AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTT
GCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT
ACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATT
ATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTGCGCAAATCAA
TCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCA
CCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTA
GATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAG
ACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAG
CGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGA
AGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAG
GCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGA
TCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCC
TCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCAC
TGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTAC
TCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTC
AACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAAC
GTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAA
CCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTG
AGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTT
GAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTC
ATGACATTAACCTATAAAAATAGGCGT

FIG._11C-2

FIG._12A

(1) C12ScFas Survival construct

C12ScFas: epsilon-cFas(CD95)-Ires-Hygro-BGH PolyA put into C12s vector backwards so that no leaky transcription happens through the cmv promoter.

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atcacgaggccccttcgtctcttcaagaacagcttgtctcttaggagttcctaatacatcccaaactcaaatatataaagc
attgacttgttctatgccctagttattaatcaattacgggtcattagttcatagcccatatatggagttccg
cgttacataacttacggtaaatgccctgctgaccgcccaacgacccccattgacgtcaataatgacgtatg
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catgacccttatgggactttcctacttggcagtacatctacgtattagtcatcgctattaccatggtgatgcggttttggc
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tctcctctgagtgttgactactccgtcagcgggggtcttcacttatcgtctgtctgcggcaactatctgtcttcggggat
ggaccaccgaccaccacggggaggtaagtggccagcaactagctagctgggtactagttagtcccaggcggccgtgaaatatcgga
tttatgcggccgcggtcggtactagttagtcgtgtactagtctctgtatctgcggacccgtggtggaactgacgagttcggaa
cacccggccgcaaccccctcggggagactcgggggaccttttggtgggccgtctcggtgccgcgcgtaaaacagttcc
tcgtttgactcctttgtgtgtgcacccccctagagaggaggggatatgtgtggtctggttctggttccgcgcgcgtaaaacagttcc
cgcctccgtccgtctgaattttgttttcggttttggggaccgaagccgccgggccgagtctctgtgtctgtctcctggtctgtgt
tgtctctgtctctgactgtgttttctgtattttgtctgtgaaaatatggccgccgtgcctcacctccacctccctaagttgac
cttagtcactggaaagatgtcgagcggatcgctcacaacagtcggtagtgcgcagcggccgagaccttcaccaccaggttaag
gctctgcagaatgccaacctttaacgtcggatggtcgcggcaccagaccagtccctcctcttaaccgagaccttggaagccttgcttttga
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ccccccgggcccctttgggtcaagccccgctcgacccccgctctttatcagcccctgaaacttccctgaccctgtcccc catat
aacctcctcgttcgaccccgcctccctttatcgggctccccctgtaaacttccctgacctgtcccctctctct
gagatcttatatgggctcacccgcacccccctcctctctgactcctctactttagtccagtcagtcccgagaagtctcgggtctcgatacccctct
ccaagctcacttacagctctctcacccttaccggtcggccgacacagtgtgtgctccgcgcaaagtggtgtccgccgacacctagaacct
accgaccggtacctcacccttaccggtcggccgacacccccaccgcgccctcaaagtggtgtccgccgacagacggcatcgacacgc
cgcccacgtgaaggctgcccggacccccgggggtggaccatcctctagactgccGGATCTCGAGGATCTCCCAGCATGCC
```

TGCTATTGTCTTCCCAATCCTCCCCCCCTTGCTGTCCTGCCCCCTCACCCCCCAGAATGACACCTACTCAGACAA

TGCGGATGCAATTTCCTCATTTTATTAGGAAAGGACAGTGGGAGTGGCACCTTCCAGGTCAAGGAAGGCACGGGGGAGGG

GCAAACAACAGATGGCTGGCAACTAGAAGGCACAGTCGAGGtCTAGCTTGCCAAACCTACAGGTGGGGTCTTTCATTCCC

FIG._12B

CCCTTTTCTCGGAGACTAAATAAAATCTTTTATTTatcgatagatcccggtcggcatctactctattccttgccctcg
gacgagtgctgctcggggcgtcggttccactatcggcgagtacttctacacagccatcggtccagacggccgcttctgcgg
gcgatttgtgtacgccgacagtcccggctccggatcggacgattgcgtcgcatcgagcatacgcgccaagctgcatcatc
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cctgcgcgacggacgccatgtagtgtattgaccgacgttcgtcgtcgatcctgcgcgccgctctgctctgctcctgcgcaggtctctgcaacgtgacac
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agcgatcgcatccatcggcgcggagatgcaatagctcaggctctcgctaaattcccatccgcaggctcctgcgcaggacatatccacg
cctgtgcacggcgcggagatgtcgataaacatacgatctttgtagaaaccatcggcgcgagctgcatcagtctggacacgctgtgcaacttt
ccctcctacatcgaagctcggaacgacgtcgcggttcagttcagcgacatcatcggctttttcagcgtcttttcaaggaaaac
cgatcagaaacttctcgacagacgtcgcggttcagttcagcgaggttttttaacctcgactaaacacagtaaaagcgcttgagagccccag
cacgtccccgtggttcggggggcctagacgttcggttacctctggcatcctcagcccttgttgtgccgtcaaagggtcgctacagacgttgtatcttatacacgcttttgg
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cgcagaggcaccctgtccgtcaggtgggggttccgctacagacgttcggttacctctggcatccct caggttgtgccgtcaaagggtcgctgcaaagggtcgctgcaaagggtcgctgcaaagggtcgctgcaaagggtcgctgcaaagggt
ttCCAGAGGAACTGCTTCCTTCCTTCACGACGACACATTCAACACAGACCTTGCATTCAACAGACCTTTGGGCGCATTCCTTTGGCGCATTCCTTTGGCGCCCCTAGACTAGA

ccaagctttggatttcattctgaagtttgaatttctgagtcactagtaatgtcttgaggatgatagtctgaattttc
tctgcaagagtacaaagattggcttttttgagatcttaatcaatgtgtcatacgcttcttcttcttcccatgaagttgatg
ccaattacgaagcagtgaacttgaacttgacttttctgctgtcttgctcatcctgatctcatctatttggcttcat
tgacaccattcttcgaacaagcctttaacttagtgtcatgactccagcaatagtggtgatatattactcaag
tcaacatcagataaatttattgccactgtttcttcttctcttcaggattttaaggttggagattcatgagaacctggttttccttctgtg
ctttctgcatgtttctgtactcttccttcttctcctttCCTGCAGTTTGTTCCTGCAGTTTGTTCCTGCAGTTTGTTCACAGCCGC
ccaaccggTTTCTGGGACTTTGTTCCTTCACGACGACACAGTGTTCACAGCCGCGAACACACAGTGTTCACAGCCGC

GAGGCGCAGCGAACACACAGTGTTCACAGCCGCGAACATCGCAGGAGAATCGCAGGAGAGAGTCTGGTTTGCACTTGCACTTGTTTGCACTTGCACTTGTATTCTGGT

CAGGGTGCAGTTGTTCCACTTCTAAACCATGCTCTTCATCGCAGAGTGTGCATCTTCTGCATTTATCAGCATAAATGGT

TCTTGTCCATGTACTCCCTTCCCTTCTGTGCATGGGCACACAGGTTGGTGTACCCCCATTCATTTGCACTTCCTCAACTTTT

TTTTTACCAGGTTGGCATGGTTGACAGCAGGTTGACAGCAAAAATGGGCCTCCTTGATATAAATCCTTCTGAGCAGTTTTTATCAGTTTCATG

AACCCCGCTCCCTCCAGCTTTAAACTCTCGGAGATGCTATTAGTAGTACCTTGAGTATGAACTCTTAACTGTGAGCCAGCAAGCA

FIG._12C

SEQ ID NO: 99960

CCAGAGGCAGGAGCAGCCCAGATCCACACCACCATGgTGGCTTTACCAACAGTACCGGAATGCCAAGCTTGCGGCCGCTTAAGA

GCTGTAATTGAACCTGGGAGTGGACACCTGTGGAGAGAAAGGCAAAGTGGATGTCAGTAAGACCAATAGGTGCCTATCAG

AAACGCAAGAGTCTTCTCTGTCTCGACAAGCCCAGTTTCTATTGGTCTCCTTAAACCTGTCTTGTAACCTTGATACTTAC

CTGCCCCAGTGCCTCACGACCAACTTctgcaggaattcctggacagctcccagatgatcagtaaccgttggtgtttattct
gtgccgggcagtggacctgggagccctgggtaggggggagctctgctttcagtgcttcagtgggtgggaaccccCaggagg
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cgcactgaggtgaactggcccctcggggGcgccctgcggggGcgcgtgtcccagatgtgtgtgcaggcgcgcagccctcgtcc
ctgtgacccgcgcttggagctgcgcaccctgagtggtggtgggcctcacCTTGTACTCACTGTCCTcgacGCGGCC

GCTCGACgataAAAATAAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAg

ctagcTTAAGTAACCCATTTGCAAGGCATGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCGGAACAG

ATGGAACAGGCAATAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGCTTGTCGGTCTCCGCTGTTCCTCGGCTCTGGGGTCTCCTCTGAGTGATTGA

TGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCCGCTTGTCCGCTGTTCCTGGGAGGGTCTCCTCTGAGTGATTGA

CTACCCGTCAGCGGGGGTCTTTCAcatgcagGCATGTATCAAAATTAATTTGGTTTTTTTTCTTAAGTATTACATTAAAT

GGCCATagttcGTAATCATGGTCATAGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG

CCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCT

TTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCG

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AAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG

GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCC

FIG._12D

TGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTC

AGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGG

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FIG._13A

(2) Ahhhh: Survival construct

2.) Ahhhh: epsilon-cFas' (CD8 or mLyt2)-Ires-Hygro-BGHpolyA also in C12s backwards

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FIG._13B

FIG._13C

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FIG._13D